

SEQUENCE LISTING

<110> Luo, Ying
Chan, Eva
Xu, Xiang
Huang, Betty
Ossovskaya, Valeria

<120> Tankyrase H, Compositions Involved in the Cell Cycle and Methods of Use

<130> RIGL-010CIP3

<140> Unassigned
<141> 2003-07-08

<150> US 09/843,159

<151> 2001-04-25

<150> US 09/696,668

<151> 2000-10-25

<150> US 09/427,154

<151> 1999-10-25

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 3797

<212> DNA

<213> Homo sapiens

<400> 1
 ctggatttc atactttgc ctggggttat ctctctgtgt ctcaactacat 60
 agacaataat tagctgtgag cagatctttt tttgttgctt cttgttagtcc cccagtttag 120
 cagaaacatt ctgttagata gatgtggaa agaattcta gcaagagttt tgcactgtat 180
 tcataagggtt gtgatttaca tatTTAAGTT ttatctttt aacatctgaa aatgtataca 240
 tactaaataat gcagaactctt attgttagt gagaacatt tgaactttga gctttcagtc 300
 acttattttt tattctttt ttgaggtagt cagtagtacc acccaaggca ctgcttaggt 360
 accactgctg cttagtggag agtcctctg gctttatcat taaggTTTg ggcggaaaga 420
 cgtagttgaa tatttgcttc agaatggtgc aagtgtccaa gcacgtgatg atgggggcct 480
 tattcctctt cataatgcat gctctttgg tcatgctgaa gtagtcaatc tcctttgcg 540
 acatggtgca gaccccaatg ctcgagataa ttggaaattat actcctctcc atgaagctgc 600
 aattaaagga aagattgtat tttgcattgt gctgttacag catggagctg agccaaaccat 660
 ccgaaataca gatggaaagga cagcattgga tttagcagat ccatctgcca aagcagtgt 720
 tactggtaaa tataagaaag atgaactctt agaaagtgcc aggagtggca atgaagaaaa 780
 aatgtatggct ctactcacac cattaaatgt caactgccac gcaagtgatg gcagaaagtc 840
 aactccattt catttggcag caggatataa cagagtaaaat attgtacagc ttttactgca 900
 acatggagct gatgtccatg ctaaaatgaa aggtgatctg gtaccattac acaatgcctg 960
 ttctttaggt cattatgaag taactgaaact tttggtaaag catgggcctt gtgtaaatgc 1020
 aatggacttg tggcaattca ctccctttca tgaggcagct tctaagaaca gggttgaagt 1080
 atgttctttt ctcttaagtt atggcaga cccaaacactg ctcaattgtc acaataaaag 1140
 tgctatagac ttggctccca caccacagtt aaaagaaaga tttagcatatg aatttaaagg 1200
 ccaactgttgc ctgcaagctg cacgagaagc tgatgttact cgaatcaaaa aacatcttc 1260
 tctggaaatg gtgaatttca agcatcctca aacacatgaa acagcattgc attgtgctgc 1320
 tgcatttcca tatccccaaa gaaagcaat atgtgaactg ttgctaaaga aaggagcaaa 1380
 catcaatgaa aagactaaag aattcttgac tcctctgcac gtggcatctg agaaagctca 1440
 taatgtatgtt gttgaagtag tggtaaaaca tgaagcaaag gttaatgctc tggataatct 1500
 tggtcagact tctctacaca gagctgcata ttgtggcat ctaacaaactt gcccctact 1560
 cctgagctat ggggtgtgatc ctaacattat atcccttcag ggctttactg cttagat 1620
 gggaaatgaa aatgtacagc aactcctcca agagggtatc tcattagta attcagaggc 1680

agacagacaa ttgctggaag ctgcaaaggc tggagatgtc gaaactgtaa aaaaactgt	1740
taçtgttçag ağtgtcaact gcagagacat tgaagggcgt cagtctaacac cacttcattt	1800
tgcagctggg tataacagag tgtccgtggt gaaatatctg ctacagcatg gagctgatgt	1860
gcatgtctaaa gataaaggag gccttgcacc tttgcacaat gcatgttctt atggacattt	1920
tgaagttgca gaacttcttg ttaaacatgg ağcagtagtt aatgtagctg atttatggaa	1980
atttacacçt ttacatgaag cagcagcaaa aggaaaatat gaaatttgca aacttctgct	2040
ccagcatggt gcagacccta ccaaaaaaaaaa cagggatgga aatactcctt tggatcttgt	2100
taaagatgga gatacagata ttcaagatct gcttägggga gatgcagctt tgctagatgc	2160
tgccaaagaag ggttggtag ccagagtgaa gaagttgtct tctcctgata atgtaaattt	2220
ccgcgataacc caäggcagac attcaacacc tttacatttgc gcaagctgggtt ataataattt	2280
agaagttgca gagtattttgt tacaacacgg agctgatgtg aatgcccag acaaaggagg	2340
acttatttcct ttacataatg cagcatcttgc cgggcatgta gatgtagcag ctctactaat	2400
aaagtataat gcatgtgtca atgcccacgg caaaatggct ttcacacçtt tgcacgaaac	2460
agcccaaaag ggaçgaaçac agcttgc tttgttgcata gcccattggag ctgacccgac	2520
tcttaaaaat caggaaggac aaacacccctt agatttagtt tcagcggatg atgtcagcgc	2580
tcttctgaca gcägcccattgc ccccatctgc tctgcctct tgttacaagc ctcaagtgt	2640
caatgggtgtg agaagcccag gagccactgc ağatgcttc tcttcaggc catctagccc	2700
atcaagccctt tctgcacccca gcaagtcttgc caacttatct gggagtttt cagaactgtc	2760
ttcagtagtt agttcaagtg gaacagaggg tgcttccagt ttggagaaaa aggaggttcc	2820
aggagtagat tttagcataa ctcaattçgt aaggaatctt ggacttgagc acctaattgg	2880
tataatttgag agagaacaga tcactttgga tttttagtt gagatggggc acaaggagct	2940
gaaggagatt ggaatcaatg ctatggaca taggcacaaa ctaattaaag gagtcgagag	3000
acttatctcc ggacaacaag gtcattaccc atatttact ttgaacaccc ctggtagtgg	3060
aacaattctt atagatçgt ctccctgatga taaagagttt cagtcgtgg aggaagagat	3120
gcaaagtaça gttcgagagc acagagatgg aggtcatgca ggtggaaatct tcaacagata	3180
caatattctc aagattcaga aggtttgtaa caagaaaacta tgggaaagat acactcaccg	3240
gagaaaaagaa gtttctgaaag aaaaccacaa ccatgccaat gaacgaaatgc tatttcatgg	3300
gtctcccttt gtgaatgcaa ttatccacaa aggctttgat gaaaggcatg cgtacatagg	3360
tggtatgttt ggagctggca tttatgttgc tggaaactct tccaaaagca atcaatatgt	3420

atatggaaatt ggaggaggta ctgggtgtcc agttcacaaa gacagatctt gttacattt 3480
ccacaggcag ctgctctttt gccggtaac cttggaaag tcttccctgc agttcagtgc 3540
aatgaaaatg gcacattctc ctccaggtca tcactcagtc actggtaggc ccagtgtaa 3600
tggcttagça ttagctgaat atgttattta cagaggagaa caggcttac 3660
aattacttac cagattatga ggcctgaagg tatggcgtat ggataaatag ttatTTtaag 3720
aaactaattc cactgaacct aaaatcatça aagcagcagt ggcctctacg ttttactcct 3780
ttgctgaaaa aaaaaaaa 3797

<210> 2

<211> 3816

<212> DNA

<213> Homo sapiens

<400> 2
cgcgctgctc cgcccgccgc ggggcagccg gggggcaggg agcccagcga ggggcgcgcg 60
tgggcgcggc ccatggact ggcgggatc cggtgacagc agggagccaa gggcccggg 120
ccctgagcgc gtcttctccg gggggcctcg ccctcctgct cgcggggccg gggctcctgc 180
tccgggtgtct ggcgtgttg ctggctgtgg cggcggccag gatcatgtcg ggtgccgct 240
gcgcggccgg gggagcggcc tgcgcgagcg cgcggccga ggcgtggag cggccgccc 300
gagagctgtt cggggcgtgc cgcaacgggg acgtggaaacg agtcaagagg ctggtgacgc 360
ctgagaaggt gaacagccgc gacacggccgg gcaggaaatc caccggctg cacttcgcgc 420
caggttttgg gcgaaagac gtatgtgaat atttgcttca gaatggtgca aatgtccaag 480
cacgtgatga tgggggcctt attcctcttc ataatgcattg ctcttttgtt catgctgaag 540
tagtcaatct cctttgcga catggtgacg accccaatgc tcgagataat tggattata 600
ctcctctcca tgaagctgca attaaaggaa agattgatgt ttgcattgtg ctgttacagc 660
atggagctga gccaaccatc cgaaatacag atgaaaggac agcattggat ttagcagatc 720
catctgccaa agcagtgcct actggtaat ataagaaaga tgaactctt aaaaagtgc 780
ggagtgccaa tgaagaaaaa atgatggctc tactcaçacc attaaatgtc aactgccacg 840
caagtgatgg cagaaagtca actccattac atttggcagc aggatataac agagtaaaga 900
ttgtacagct gttactgcaa catggagctg atgtccatgc taaagataaa ggtgatctgg 960

taccattaca	caatgcctgt	tcttatggtc	attatgaagt	aaçtgaactt	ttggtçägc	1020
atgggtgcctg	tgtaaatgca	atggacttgt	ggcaattcac	tcctcttcat	gaggcagctt	1080
ctaagaacag	ggttgaagta	tgttctcttc	tcttaagtta	tggtgcagac	ccaacactgc	1140
tcaatçtgçca	caataaaagt	gctatagact	tggctccac	accacagtta	aaagaaagat	1200
tagcatatga	attnaaaggc	cactcgttgc	tgcaagctgc	acgagaagct	gatgttactc	1260
gaatcaaaaa	acatctctct	ctggaaatgg	tgaatttcaa	gcatcctcaa	acacatgaaa	1320
cagcattgca	ttgtgctgct	gcatctccat	atcccaaaag	aaagcaaata	tgtgaactgt	1380
tgctaagaaa	aggagçäac	atcaatgaaa	agactaaaga	attcttgact	cctctgcacg	1440
tggcatctga	gaaagctcat	aatgatgtt	ttgaagtagt	ggtgaaacat	gaagcaaagg	1500
ttaatgctct	ggataatctt	ggtcagactt	ctctacacag	agctgcata	tgtggtcatc	1560
tacaaacctg	ccgcctactc	ctgagctatg	ggtgtgatcc	taacattata	tcccttcagg	1620
gctttactgc	tttaçagatg	ggaaatgaaa	atgtacagca	actcctccaa	gagggtatct	1680
cattaggtaa	ttcagaggca	gacagacaat	tgctggaagc	tgcaaaggct	ggagatgtcg	1740
aaactgtaaa	aaaactgtgt	actgttcaga	gtgtcaactg	cagagacatt	gaagggcgtc	1800
agtcetacacc	acttcatttt	gcagctgggt	ataacagagt	gtccgtggtg	gaatatctgc	1860
tacagcatgg	agctgatgt	catgctaaag	ataaaggagg	ccttgcac	ttgcacaatg	1920
catgttctta	tggacattat	gaagttgcag	aacttcttgt	taaacatgga	gcagtagtta	1980
atgtagctga	tttatggaaa	tttacacctt	tacatgaagc	agcagcaaaa	ggaaaatatg	2040
aaatttgcaa	acttctgctc	cagcatggtg	cagaccctac	caaaaaaaac	agggatggaa	2100
atactccttt	ggatcttgtt	aaagatggag	atacagatat	tcaagatctg	cttagggag	2160
atgcagcttt	gctagatgct	gccaagaagg	gttgtttagc	cagagtgaag	aagttgtctt	2220
ctcctgataa	tgttaattgc	cgcgatacc	aaggcagaca	ttcaacac	ttacatttag	2280
cagctggta	taataattta	gaagttgcag	agtatttgtt	acaacacgga	gctgatgtga	2340
atgcccaga	caaaggagga	cttattcctt	tacataatgc	agcatctac	ggccatgtag	2400
atgtagcägc	tctactaata	aagtataatg	catgtgtçaa	tgccacggac	aaatgggctt	2460
tcacaccttt	gcacgaagca	gcccaaagg	gacgaacaca	gctttgtgct	ttgttgctag	2520
cccatggagc	tgacccgact	cttaaaaatc	aggaaggaca	aacacctta	gatttagttt	2580
cagcggatga	tgtcagcgct	cttctgacag	cagccatgcc	cccatctgct	ctgccccttt	2640
gttacaagcc	tcaagtgc	aatggtgtga	gaagcccägg	agccactgca	gatgtctct	2700

cttcagggcc atctagccca tcaaggcctt ctgcagccag cagtcgtac aacttatctg 2760
 ggagttttc agaactgtct tcagtagtta gttcaagtgg aacagagggt gcttccagtt 2820
 tggagaaa ggaggttcca ggagtagatt ttagcataac tcaattcgta aggaatctg 2880
 gacttgcac cctaattggat atatttgaga gagaacagat cacttggat gtatttagtt 2940
 agatggggca caaggagctg aaggagattg gaatcaatgc ttatggacat aggcacaaac 3000
 taattaaagg agtcgagaga cttatctccg gacaacaagg tcttaaccca tatttaactt 3060
 tgaacacccctc tggtagtggc acaattctta tagatctgtc tcctgatgtaaagagttc 3120
 agtctgtgga ggaagagatg caaagtacag ttcgagagca cagagatgg ggtcatgcag 3180
 gtggaatctt caacagatac aatattctca agattcagaa ggttgtaac aagaaactat 3240
 gggaaagata cactcaccgg agaaaagaag tttctgaaga aaaccacaaac catgccaatg 3300
 aacgaatgct atttcatggg tctcccttttgc tgaatgcaat tattccacaaa ggctttgatg 3360
 aaaggcatgc gtacataggt ggtatgtttg gagctggcat ttatgttgc gaaaactctt 3420
 ccaaagcaa tcaatatgta tattggattt gaggaggtac tgggtgtcca gttcacaaag 3480
 acagatcttgc ttacatttgc cacaggcagc tgctcttttgc ccgggttaacc ttggaaagt 3540
 ctcccttgca gttcagtgc atgaaaatgg cacattctcc tccaggtcat cactcagtc 3600
 ctggtaggcc cagtgtaaat ggcctagcat tagctgaata tgttatattac agaggagaac 3660
 aggcttatcc tgagtattta attacttacc agattatgag gcctgaaggt atggtcgatg 3720
 gataaaatgt tattttaaaga aactaattcc actgaaccta aaatcatcaa agcagcagtg 3780
 gcctctacgt ttactcctt tgctgaaaaa aaaaaa 3816

<210> 3

<211> 1065

<212> PRT

<213> Homo sapiens

<400> 3

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala
 1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
 20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val
340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr
515 520 525

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn
545 550 555 560

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu
565 570 575

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu
580 585 590

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp
595 600 605

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn
610 615 620

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn
625 630 635 640

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr
645 650 655

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val
660 665 670

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln
675 680 685

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp
690 695 700

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser
705 710 715 720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser
755 760 765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu
770 775 780

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu
785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val
805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln
820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu
835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val
850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu
865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp
885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Met Gln Ser Thr Val Arg Glu
900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile
915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr
930 935 940

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu
945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys
965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly
980 985 990

Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly
995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val
1055 1060 1065

<210> 4

<211> 1240

<212> PRT

<213> Homo sapiens

<400> 4

Arg Cys Ser Ala Arg Arg Gly Ala Ala Gly Gly Gln Gly Ala Gln Arg
1 5 10 15

Gly Ala Arg Val Gly Ala Ala His Gly Thr Ala Pro Asp Pro Val Thr
20 25 30

Ala Gly Ser Gln Ala Ala Arg Ala Leu Ser Ala Ser Ser Pro Gly Gly
35 40 45

Leu Ala Leu Leu Ala Gly Pro Gly Leu Leu Leu Arg Leu Leu Ala
50 55 60

Leu Leu Leu Ala Val Ala Ala Ala Arg Ile Met Ser Gly Arg Arg Cys
65 70 75 80

Ala Gly Gly Ala Ala Cys Ala Ser Ala Ala Glu Ala Val Glu
85 90 95

Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn Gly Asp Val Glu
100 105 110

Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn Ser Arg Asp Thr
115 120 125

Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala Gly Phe Gly Arg
130 135 140

Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala Asn Val Gln Ala
145 150 155 160

Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala Cys Ser Phe Gly
165 170 175

His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly Ala Asp Pro Asn
180 185 190

Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu Ala Ala Ile Lys
195 200 205

Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His Gly Ala Glu Pro
210 215 220

Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp Leu Ala Asp Pro
225 230 235 240

Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys Asp Glu Leu Leu
245 250 255

Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met Ala Leu Leu Thr
260 265 270

Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg Lys Ser Thr Pro
275 280 285

Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile Val Gln Leu Leu
290 295 300

Leu	Gln	His	Gly	Ala	Asp	Val	His	Ala	Lys	Asp	Lys	Gly	Asp	Leu	Val	
305																320
310																315
Pro	Leu	His	Asn	Ala	Cys	Ser	Tyr	Gly	His	Tyr	Glu	Val	Thr	Glu	Leu	
																335
																325
																330
Leu	Val	Lys	His	Gly	Ala	Cys	Val	Asn	Ala	Met	Asp	Leu	Trp	Gln	Phe	
																350
																340
																345
Thr	Pro	Leu	His	Glu	Ala	Ala	Ser	Lys	Asn	Arg	Val	Glu	Val	Cys	Ser	
																355
																360
																365
Leu	Leu	Leu	Ser	Tyr	Gly	Ala	Asp	Pro	Thr	Leu	Leu	Asn	Cys	His	Asn	
																370
																375
																380
Lys	Ser	Ala	Ile	Asp	Leu	Ala	Pro	Thr	Pro	Gln	Leu	Lys	Glu	Arg	Leu	
																385
																390
																395
																400
Ala	Tyr	Glu	Phe	Lys	Gly	His	Ser	Leu	Leu	Gln	Ala	Ala	Arg	Glu	Ala	
																405
																410
																415
Asp	Val	Thr	Arg	Ile	Lys	Lys	His	Leu	Ser	Leu	Glu	Met	Val	Asn	Phe	
																420
																425
																430
Lys	His	Pro	Gln	Thr	His	Glu	Thr	Ala	Leu	His	Cys	Ala	Ala	Ala	Ser	
																435
																440
																445
Pro	Tyr	Pro	Lys	Arg	Lys	Gln	Ile	Cys	Glu	Leu	Leu	Leu	Arg	Lys	Gly	
																450
																455
																460
Ala	Asn	Ile	Asn	Glu	Lys	Thr	Lys	Glu	Phe	Leu	Thr	Pro	Leu	His	Val	
																465
																470
																475
																480
Ala	Ser	Glu	Lys	Ala	His	Asn	Asp	Val	Val	Glu	Val	Val	Val	Lys	His	
																485
																490
																495
Glu	Ala	Lys	Val	Asn	Ala	Leu	Asp	Asn	Leu	Gly	Gln	Thr	Ser	Leu	His	
																500
																505
																510
Arg	Ala	Ala	Tyr	Cys	Gly	His	Leu	Gln	Thr	Cys	Arg	Leu	Leu	Leu	Ser	
																515
																520
																525

Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly Phe Thr Ala Leu
530 535 540

Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln Glu Gly Ile Ser
545 550 555 560

Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu Ala Ala Lys Ala
565 570 575

Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val Gln Ser Val Asn
580 585 590

Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu His Phe Ala Ala
595 600 605

Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu Gln His Gly Ala
610 615 620

Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro Leu His Asn Ala
625 630 635 640

Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu Val Lys His Gly
645 650 655

Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr Pro Leu His Glu
660 665 670

Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu Leu Gln His
675 680 685

Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn Thr Pro Leu Asp
690 695 700

Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu Leu Arg Gly Asp
705 710 715 720

Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu Ala Arg Val Lys
725 730 735

Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp Thr Gln Gly Arg
740 745 750

His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Asn Leu Glu Val
755 760 765

Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn Ala Gln Asp Lys
770 775 780

Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr Gly His Val Asp
785 790 795 800

Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val Asn Ala Thr Asp
805 810 815

Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln Lys Gly Arg Thr
820 825 830

Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp Pro Thr Leu Lys
835 840 845

Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser Ala Asp Asp Val
850 855 860

Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala Leu Pro Ser Cys
865 870 875 880

Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro Gly Ala Thr Ala
885 890 895

Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser Leu Ser Ala Ala
900 905 910

Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu Leu Ser Ser Val
915 920 925

Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu Glu Lys Lys Glu
930 935 940

Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val Arg Asn Leu Gly
945 950 955 960

Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln Ile Thr Leu Asp
965 970 975

Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu Ile Gly Ile Asn
980 985 990

Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val Glu Arg Leu Ile
995 1000 1005

Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu Asn Thr Ser
1010 1015 1020

Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp Lys Glu
1025 1030 1035

Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val Arg Glu His
1040 1045 1050

Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile
1055 1060 1065

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr
1070 1075 1080

Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala
1085 1090 1095

Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile
1100 1105 1110

Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met
1115 1120 1125

Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn
1130 1135 1140

Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His
1145 1150 1155

Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys
1160 1165 1170

Arg Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys
1175 1180 1185

Met Ala His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro
1190 1195 1200

Ser Val Asn Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly
1205 1210 1215

Glu Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg
1220 1225 1230

Pro Glu Gly Met Val Asp Gly
1235 1240

<210> 5

<211> 61

<212> DNA

<213> Homo sapiens

<400> 5

gtggaacaga gggtgcttcc agtttgaga aaaaggaggt tccaggagta gattttagca 60

t 61

<210> 6

<211> 61

<212> DNA

<213> Homo sapiens

<400> 6

atgcagggga tggcgccgag ggaacagaaa ggaaggaagg agaagttgct ggtcttgaca 60

t 61

<210> 7

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic

<400> 7

gtggaacaga gggtgcttcc

20

<210> 8

<211> 1100

<212> PRT

<213> Homo sapiens

<400> 8

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala
1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val
340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr
515 520 525

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn
545 550 555 560

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu
565 570 575

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu
580 585 590

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp
595 600 605

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn
610 615 620

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn
625 630 635 640

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr
645 650 655

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val
660 665 670

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln
675 680 685

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp
690 695 700

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser
705 710 715 720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser
755 760 765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu
770 775 780

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu
785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val
805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln
820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu
835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val
850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu
865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp
885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Met Gln Ser Thr Val Arg Glu
900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile
915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr
930 935 940

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu
945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys
965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly
980 985 990

Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly
995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
1055 1060 1065

Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro
1070 1075 1080

Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
1085 1090 1095

Asp Gly
1100

<210> 9

<211> 338

<212> PRT

<213> Homo sapiens

<400> 9

Arg Cys Ser Ala Arg Arg Gly Ala Ala Gly Gly Gln Gly Ala Gln Arg
1 5 10 15

Gly Ala Arg Val Gly Ala Ala His Gly Thr Ala Pro Asp Pro Val Thr
20 25 30

Ala Gly Ser Gln Ala Ala Arg Ala Leu Ser Ala Ser Ser Pro Gly Gly
35 40 45

Leu Ala Leu Leu Leu Ala Gly Pro Gly Leu Leu Leu Arg Leu Leu Ala
50 55 60

Leu Leu Leu Ala Val Ala Ala Arg Ile Met Ser Gly Arg Arg Cys
65 70 75 80

Ala Gly Gly Gly Ala Ala Cys Ala Ser Ala Ala Glu Ala Val Glu
85 90 95

Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn Gly Asp Val Glu
100 105 110

Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn Ser Arg Asp Thr
115 120 125

Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala Gly Phe Gly Arg
130 135 140

Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala Asn Val Gln Ala
145 150 155 160

Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala Cys Ser Phe Gly
165 170 175

His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly Ala Asp Pro Asn
180 185 190

Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu Ala Ala Ile Lys
195 200 205

Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His Gly Ala Glu Pro
210 215 220

Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp Leu Ala Asp Pro
225 230 235 240

Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys Asp Glu Leu Leu
245 250 255

Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met Ala Leu Leu Thr
260 265 270

Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg Lys Ser Thr Pro
275 280 285

Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile Val Gln Leu Leu
290 295 300

Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Asp Leu Val
305 310 315 320

Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Thr Glu Leu
325 330 335

Leu Val

<210> 10

<211> 583

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic mutant

<400> 10

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala
1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
210 215 220

Glu	Val	Cys	Ser	Leu	Leu	Leu	Ser	Tyr	Gly	Ala	Asp	Pro	Thr	Leu	Leu
225															240
Asn	Cys	His	Asn	Lys	Ser	Ala	Ile	Asp	Leu	Ala	Pro	Thr	Pro	Gln	Leu
															255
Lys	Glu	Arg	Leu	Ala	Tyr	Glu	Phe	Lys	Gly	His	Ser	Leu	Leu	Gln	Ala
															270
Ala	Arg	Glu	Ala	Asp	Val	Thr	Arg	Ile	Lys	Lys	His	Leu	Ser	Leu	Glu
															285
Met	Val	Asn	Phe	Lys	His	Pro	Gln	Thr	His	Glu	Thr	Ala	Leu	His	Cys
															290
Ala	Ala	Ala	Ser	Pro	Tyr	Pro	Lys	Arg	Lys	Gln	Ile	Cys	Glu	Leu	Leu
															305
Leu	Arg	Lys	Gly	Ala	Asn	Ile	Asn	Glu	Lys	Thr	Lys	Glu	Phe	Leu	Thr
															320
325															335
Pro	Leu	His	Val	Ala	Ser	Glu	Lys	Ala	His	Asn	Asp	Val	Val	Glu	Val
															340
															345
Val	Val	Lys	His	Glu	Ala	Lys	Val	Asn	Ala	Leu	Asp	Asn	Leu	Gly	Gln
															355
355															360
360															365
Thr	Ser	Leu	His	Arg	Ala	Ala	Tyr	Cys	Gly	His	Leu	Gln	Thr	Cys	Arg
															370
															375
Leu	Leu	Leu	Ser	Tyr	Gly	Cys	Asp	Pro	Asn	Ile	Ile	Ser	Leu	Gln	Gly
															385
															390
Phe	Thr	Ala	Leu	Gln	Met	Gly	Asn	Glu	Asn	Val	Gln	Gln	Leu	Leu	Gln
															405
															410
Glu	Gly	Ile	Ser	Leu	Gly	Asn	Ser	Glu	Ala	Asp	Arg	Gln	Leu	Leu	Glu
															420
															425
															430
Ala	Ala	Lys	Ala	Gly	Asp	Val	Glu	Thr	Val	Lys	Lys	Leu	Cys	Thr	Val
															435
															440
															445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr
515 520 525

Pro Leu His Glu Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Thr Gly Met Glu Ile
545 550 555 560

Leu Leu Trp Ile Leu Leu Lys Met Glu Ile Gln Ile Phe Lys Ile Cys
565 570 575

Leu Gly Glu Met Gln Leu Cys
580

<210> 11

<211> 1100

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic mutant

<400> 11

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala
1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Arg His Gly
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
145 150 155 160

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
210 215 220

Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val
340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu			
500	505	510	
Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr			
515	520	525	
Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu			
530	535	540	
Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn			
545	550	555	560
Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu			
565	570	575	
Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu			
580	585	590	
Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp			
595	600	605	
Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn			
610	615	620	
Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn			
625	630	635	640
Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr			
645	650	655	
Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val			
660	665	670	
Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln			
675	680	685	
Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp			
690	695	700	
Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser			
705	710	715	720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser
755 760 765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu
770 775 780

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu
785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val
805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln
820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu
835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val
850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu
865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp
885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Met Gln Ser Thr Val Arg Glu
900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile
915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr
930 935 940

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu
945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys
965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly
980 985 990

Ile Tyr Leu Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly
995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
1055 1060 1065

Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Gln Ala Tyr Pro
1070 1075 1080

Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
1085 1090 1095

Asp Gly
1100

<210> 12

<211> 1083

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic mutant

<400> 12

Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn Gly Ala
1 5 10 15

Ser Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
20 25 30

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly
35 40 45

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
50 55 60

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
65 70 75 80

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
85 90 95

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
100 105 110

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
115 120 125

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
130 135 140

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
145 150 155 160

Val Gln Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
165 170 175

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
180 185 190

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
195 200 205

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
210 215 220

Glu Val Cys Ser Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu
225 230 235 240

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu
245 250 255

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala
260 265 270

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu
275 280 285

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys
290 295 300

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu
305 310 315 320

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr
325 330 335

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val
340 345 350

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln
355 360 365

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg
370 375 380

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly
385 390 395 400

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln
405 410 415

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu
420 425 430

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val
435 440 445

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
450 455 460

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
465 470 475 480

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
485 490 495

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu
500 505 510

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr
515 520 525

Pro Leu His Glu Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu
530 535 540

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn
545 550 555 560

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu
565 570 575

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu
580 585 590

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp
595 600 605

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn
610 615 620

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn
625 630 635 640

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr
645 650 655

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val
660 665 670

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln
675 680 685

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp
690 695 700

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser
705 710 715 720

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala
725 730 735

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro
740 745 750

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser
755 760 765

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu
770 775 780

Leu Ser Ser Val Val Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu
785 790 795 800

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val
805 810 815

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln
820 825 830

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu
835 840 845

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val
850 855 860

Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu Thr Leu
865 870 875 880

Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro Asp Asp
885 890 895

Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val Arg Glu
900 905 910

His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr Asn Ile
915 920 925

Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg Tyr Thr
930 935 940

His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His Ala Asn Glu
945 950 955 960

Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala Ile Ile His Lys
965 970 975

Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly Met Phe Gly Ala Gly
980 985 990

Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser Asn Gln Tyr Val Tyr Gly
995 1000 1005

Ile Gly Gly Gly Thr Gly Cys Pro Val His Lys Asp Arg Ser Cys
1010 1015 1020

Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg Val Thr Leu Gly
1025 1030 1035

Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala His Ser Pro
1040 1045 1050

Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn Gly Leu
1055 1060 1065

Ala Leu Ala Ala Tyr Val Ile Tyr Arg Gly Glu Gln Ala Leu Ser
1070 1075 1080

<210> 13

<211> 9

<212> PRT

<213> Unknown

<220>

<223> cyclin A destruction box

<400> 13

Arg Thr Val Leu Gly Val Ile Gly Asp
1 5

<210> 14

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Cyclin B1 destruction box

<400> 14

Arg Thr Ala Leu Gly Asp Ile Gly Asn
1 5

<210> 15

<211> 27

<212> PRT

<213> Rattus sp.

<400> 15

Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
1 5 10 15

Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
20 25

<210> 16

<211> 28

<212> PRT

<213> Mus sp.

<400> 16

Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
1 5 10 15

Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
20 25

<210> 17

<211> 27

<212> PRT

<213> Mus sp.

<400> 17

Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg
1 5 10 15

Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
20 25

<210> 18

<211> 27

<212> PRT

<213> Mus sp.

<400> 18

Asp Arg Phe Leu Gln Ala Gln Leu Val Cys Arg Lys Lys Leu Gln Val
1 5 10 15

Val Gly Ile Thr Ala Leu Leu Leu Ala Ser Lys
20 25

<210> 19

<211> 18

<212> PRT

<213> Mus sp.

<400> 19

Met Ser Val Leu Arg Gly Lys Leu Gln Leu Val Gly Thr Ala Ala Met
1 5 10 15

Leu Leu